A PROTEIN INVOLVED IN CARCINOMA

The present invention relates to methods for the treatment and/or prophylaxis of carcinoma, in particular liver cancer, stomach cancer and/or colon cancer comprising targeting of the polypeptide MAL2, agents which interact with or modulate the expression or activity of the polypeptide, methods for the identification of such agents and the use of MAL2 in the diagnosis of carcinoma, in particular stomach, colon and/or liver cancer.

There are three main types of stomach cancers: lymphomas, gastric stromal tumours, and carcinoid tumours. Lymphomas are cancers of the immune system tissue that are sometimes found in the wall of the stomach. Gastric stromal tumours develop from the tissue of the stomach wall. Carcinoid tumours are tumours of hormone-producing cells of the stomach. Stomach cancers can grow slowly and imperceptibly with symptoms sometimes only developing once the disease has spread beyond the stomach, for example to involve the liver. Thus, it is often many months from the time that symptoms first appear to the patient seeking medical advice. This delay may allow time for the tumour to spread and to progress from being potentially curable to being inoperable. The major treatments are aggressive and debilitating. Hence, there is a need for new targets for the treatment of, and markers for earlier diagnosis of stomach cancer.

Tumour specific proteins have been identified for a number of cancer types using techniques such as differential screening of cDNAs (Hubert, R.S., *et al.*, 1999, Proc. Natl. Acad. Sci. USA 96:14523-14528) and the purification of cell-surface proteins that are recognised by tumour-specific antibodies (Catimel, B., *et al.*, 1996, J. Biol. Chem. 271: 25664-25670). More recently, DNA 'chips' containing up to 10,000 expressed sequence elements have been used to characterise tumour cell gene expression (Dhanasekaran, S.M., *et al.*, 2001, Nature 412:822-826). However, there are several reasons why the numerous and extensive previous transcriptomic analysis of cancers may not have revealed all, or even most, tumour associated proteins. These include: (i) a lack of correlation between transcript and disease-associated protein levels, particularly common for membrane proteins that often have a long half-life and as such do not have a high mRNA turnover. Therefore, whilst the difference in protein levels between normal and cancerous cells are consistent it is often difficult to associate changes in the mRNA for a given membrane protein with the cancerous state. (ii) Translocation of a protein in the disease state rather than simply differential levels of the transcript, for example, erbB2/HER2-neu, shows much greater plasma-membrane localisation in cancer cells than normal breast cells, and the transcription factors oestrogen receptor and STAT3 translocate to the nucleus to exert their tumourigenic effects. (iii) Novel,

uncharacterised genes are not highly represented within the 'closed system' of a cDNA array where there are restrictions on the number of expressed sequence elements per chip and the knowledge and availability of DNA clones. It is well established that there is an unreliable relationship between protein expression and mRNA levels (*e.g.* Gygi SP *et al.*, Mol. Cell Biol. 1999, 19:1720-30) as protein expression is subject to strict translational control at several levels. Regulation of the overall activity of the translational apparatus of a cell is expected to affect the translation of essentially all mRNAs (Matthews, M. *et al.*, in Translational Control by Hershey, J. *et al.*, pp 11-12, Cold Spring Harbour laboratory Press, 1996). Indeed, a fraction of specific mRNA is completely repressed. Furthermore individual mRNAs differ greatly in their efficiencies of translation and can be 'weak' or 'strong', thus contributing to the regulation of gene expression. Thus, the existence of a conceptual translation of a cDNA cannot provide definitive evidence of the existence of a particular protein in a particular cell type.

There are two main types of liver cancer; hepatoma, also known as hepatocellular carcinoma, is the most common type of primary liver cancer and accounts for around 85% of all primary liver cancers. It develops from the main liver cells called hepatocytes. Cholangiocarcinoma arises in the cells that line the bile duct and it accounts for around 12% of primary liver cancers. The main treatments for primary liver cancer are surgery and chemotherapy with surgical removal considered to be the most effective treatment. Unfortunately, about 70% of patients cannot have this surgery due the size or location of the tumours or other health factors. Thus, important needs exist for new therapeutic agents for the treatment of liver cancer.

Colon cancer is a leading cancer killer of both men and women with a large proportion of cases diagnosed during later stages of the disease. Surgery is the main treatment for colorectal cancer. Radiation therapy is often used after surgery and adjuvant chemotherapy may also be used. Carcinoembryonic antigen (CEA) and CA 19-9 are substances produced by cells of most colon and rectal cancers and released into the bloodstream. These markers, however, can be high for reasons other than cancer, or can be normal in a person who has cancer. Thus, important needs exist for new therapeutic agents for the treatment of colon cancer. Additionally, there is a clear need to identify new colon cancer-associated proteins for use as sensitive and specific biomarkers for the diagnosis of colon cancer in living subjects.

Breast cancer is the most frequently diagnosed cancer in women. The implementation of screening programs for the early detection of breast cancer, and the advent of anticancer

treatments, such as chemotherapy, radiotherapy and anti-oestrogen therapies, to augment surgical resection have improved the survival of breast cancer patients. However, some breast tumours become refractory to such treatments, as the cancer cells develop resistance to chemotherapy drugs or lose their hormone sensitivity, leading to recurrent or metastatic disease which is often incurable. More recently, attention has focussed on the development of immunological therapies (Green, MC. *et al.*, 2000, Cancer Treat. Rev. 26:269-286; Davis, ID., 2000, Immunol. Cell Biol. 78:179-195; Knuth, A. *et al.*, 2000, Cancer Chemother Pharmacol. 46:S46-51; Shiku, H. *et al.*, 2000, Cancer Chemother. Pharmacol. 46:S77-82; Saffran, DC. *et al.*, 1999, Cancer Metastasis Rev. 18:437-449), such as cancer vaccines and monoclonal antibodies (mAbs), as a means of initiating and targeting a host immune response against tumour cells. Herceptin, a mAb that recognises the erbB2/HER2-neu receptor protein, is used as a treatment for metastatic breast cancer. In combination with chemotherapy, Herceptin has been shown to prolong the time to disease progression, when compared to patients receiving chemotherapy alone (Baselga, J. *et al.*, 1998, Cancer Res. 58:2825-2831). Herceptin, however, is only effective in treating the 10-20% of patients whose tumours over-express the erbB2 protein. Thus, an increasingly important need exists to identify new breast cancer associated proteins for use as sensitive and specific biomarkers for the diagnosis of breast cancer in living subjects. Additionally, there is a clear need for new therapeutic agents for the treatment of breast cancer that work quickly, potently, specifically, and with fewer side effects.

WO 02/00677 discloses a nucleic acid encoding a 215 amino acid long polypeptide, 176 amino acids of which are identical to MAL2. WO 01/36440, and WO 02/70539 disclose a nucleic acid encoding a polypeptide identical to MAL2 but no specific utilities are disclosed. WO 01/53343 discloses multiple nucleic acids, one of which encodes a MAL2 polypeptide of use in the detection and/or treatment of diseases involving aberrant T-cell function and in endometrial, ovarian, lung and breast cancers. WO 02/71928 discloses hundreds of nucleic acids and encoding polypeptides, including one identical to MAL2, of use in the diagnosis and treatment of ovarian cancer. WO 01/22920 discloses more than 7000 nucleic acid sequences, one of which does not encode a MAL2 polypeptide but does encode a polypeptide larger than MAL2 which is 98% identical over a sequence 95% of the length of MAL2, of use in the diagnosis and/or treatment of colon cancer.

The present invention is based on the finding that MAL2 is a novel target for the therapeutic intervention of carcinoma, in particular stomach, colon and/or liver cancers.

Accordingly, the invention provides a method for the treatment and/or prophylaxis of carcinoma comprising administering a therapeutically effective amount of an agent which interacts with or modulates the expression or activity of a MAL2 polypeptide.

A MAL2 polypeptide includes a polypeptide which:

(a) comprises or consists of the amino acid sequence of SEQ ID NO:1; or

(b) is a derivative having one or more amino acid substitutions, modifications, deletions or insertions relative to the amino acid sequence of SEQ ID NO:1 which retains the activity of MAL2.

The term "polypeptides" includes peptides, polypeptides and proteins. These are used interchangeably unless otherwise specified.

In the present application, the term "carcinoma" includes a malignant new growth that arises from epithelium, found in skin or, more commonly, the lining of body organs, for example: breast, prostate, lung, kidney, pancreas, liver, stomach, bladder or colon. Carcinomas tend to infiltrate into adjacent tissue and spread (metastasise) to distant organs, for example: to bone, liver, lung or the brain. In one embodiment of the invention, the carcinoma is liver cancer. In a further embodiment, the carcinoma is stomach cancer and in yet a further embodiment, the carcinoma is colon cancer. In another embodiment, the carcinoma is breast cancer.

Agents of use in the methods of the invention include without limitation, agents that are capable of interacting with (*e.g.* binding to, or recognising) a MAL2 polypeptide or a nucleic acid molecule encoding a MAL2 polypeptide, or are capable of modulating the interaction, expression or activity of a MAL2 polypeptide or the expression of a nucleic acid molecule encoding a MAL2 polypeptide. Such agents include, without limitation, antibodies, nucleic acids (*e.g.* DNA and RNA), carbohydrates, lipids, proteins, polypeptides, peptides, peptidomimetics, small molecules and other drugs.

Thus, the invention also provides the use of an agent, which interacts with or modulates the expression or activity of a MAL2 polypeptide for the manufacture of a medicament for the treatment and/or prophylaxis of carcinoma.

Most preferably, the agent for use in the treatment and/or prophylaxis of carcinoma is an antibody which interacts with (*i.e.* binds to or recognises) or modulates the activity of a MAL2 polypeptide. Accordingly, there is provided the use of an antibody that interacts with a MAL2 polypeptide of use for the manufacture of a medicament for use in the treatment and/or prophylaxis of carcinoma. Also provided is a method of treatment and/or prophylaxis of carcinoma in a subject comprising administering to said subject a therapeutically effective

amount of an antibody which interacts with MAL2. In particular, an antibody that interacts with a MAL2 polypeptide may be used to mediate antibody dependent cell cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC). In such a case the antibody is preferably a full length naked antibody. In another aspect of the invention, an antibody that interacts with MAL2 polypeptides may be used to inhibit the activity of said polypeptides.

Most preferred are antibodies that specifically interact with a MAL2 polypeptide. Specifically interacting with (*e.g.* recognising or binding to) means that the antibodies have a greater affinity for MAL2 polypeptides than for other polypeptides.

An antibody, optionally conjugated to a therapeutic moiety, can be used therapeutically alone or in combination with a cytotoxic factor(s) and/or cytokine(s). In particular, MAL2 antibodies can be conjugated to a therapeutic agent, such as a cytotoxic agent, a radionuclide or drug moiety to modify a given biological response. The therapeutic agent is not to be construed as limited to classical chemical therapeutic agents. For example, the therapeutic agent may be a drug moiety that may be a protein or polypeptide possessing a desired biological activity. Such moieties may include, for example and without limitation, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin, a protein such as tumour necrosis factor, α-interferon, β-interferon, nerve growth factor, platelet derived growth factor or tissue plasminogen activator, a thrombotic agent or an anti-angiogenic agent, *e.g.* angiostatin or endostatin, or, a biological response modifier such as a lymphokine, interleukin-1 (IL-1), interleukin-2 (IL-2), interleukin-6 (IL-6), granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), nerve growth factor (NGF) or other growth factor.

Therapeutic agents also include cytotoxins or cytotoxic agents including any agent that is detrimental to (*e.g.* kills) cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents also include, but are not limited to, antimetabolites (*e.g.* methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.* mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.* daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.* dactinomycin (formerly actinomycin),

bleomycin, mithramycin, anthramycin (AMC), calicheamicins or duocarmycins), and anti-mitotic agents (*e.g.* vincristine and vinblastine).

Other therapeutic moieties may include radionuclides such as ^{111}In and ^{90}Y, Lu^{177}, $Bismuth^{213}$, $Californium^{252}$, $Iridium^{192}$ and $Tunsten^{188}$/$Rhenium^{188}$; or drugs such as but not limited to, alkylphosphocholines, topoisomerase I inhibitors, taxoids and suramin.

Techniques for conjugating such therapeutic agents to antibodies are well known in the art (see, *e.g.* Arnon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld *et al.*, eds., 1985 pp. 243-56, ed. Alan R. Liss, Inc; Hellstrom *et al.*, "Antibodies For Drug Delivery", in Controlled Drug Delivery, 2nd Ed., Robinson *et al.*, eds., 1987, pp. 623-53, Marcel Dekker, Inc.; Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications; Pinchera *et al.*, 1985, eds., pp. 475-506; "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabelled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin *et al.* (eds.), 1985, pp. 303-16, Academic Press; Thorpe *et al.*, 1982 "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev., 62:119-58 and Dubowchik *et al.*, 1999, Pharmacology and Therapeutics, 83, 67-123).

The antibodies for use in the invention include analogues and derivatives that are modified, for example but without limitation, by the covalent attachment of any type of molecule. Preferably, said attachment does not impair immunospecific binding. In one aspect, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate (see US 4,676,980).

In other embodiments, the invention provides the therapeutic use of fusion proteins of the antibodies (or functionally active fragments thereof), for example but without limitation, where the antibody or fragment thereof is fused via a covalent bond (*e.g.* a peptide bond), at optionally the N-terminus or the C-terminus, to an amino acid sequence of another protein (or portion thereof; preferably at least a 10, 20 or 50 amino acid portion of the protein). Preferably the antibody, or fragment thereof, is linked to the other protein at the N-terminus of the constant domain of the antibody. In another aspect, an antibody fusion protein may facilitate depletion or purification of a polypeptide as described herein, increase half-life *in vivo*, and enhance the delivery of an antigen across an epithelial barrier to the immune system.

Where the fusion protein is an antibody fragment linked to an effector or reporter molecule, this may be prepared by standard chemical or recombinant DNA procedures. A

preferred effector group is a polymer molecule, which may be attached to the modified Fab fragment to increase its half-life *in vivo*.

The polymer molecule may, in general, be a synthetic or a naturally occurring polymer, for example an optionally substituted straight or branched chain polyalkylene, polyalkenylene or polyoxyalkylene polymer or a branched or unbranched polysaccharide, e.g. a homo- or hetero- polysaccharide.

Particular optional substituents which may be present on the above-mentioned synthetic polymers include one or more hydroxy, methyl or methoxy groups. Particular examples of synthetic polymers include optionally substituted straight or branched chain poly(ethyleneglycol), poly(propyleneglycol) poly(vinylalcohol) or derivatives thereof, especially optionally substituted poly(ethyleneglycol) such as methoxypoly(ethyleneglycol) or derivatives thereof.

Particular naturally occurring polymers include lactose, amylose, dextran, glycogen or derivatives thereof.

"Derivatives" as used herein is intended to include reactive derivatives, for example thiol-selective reactive groups such as maleimides and the like. The reactive group may be linked directly or through a linker segment to the polymer. It will be appreciated that the residue of such a group will in some instances form part of the product as the linking group between the antibody fragment and the polymer.

The size of the polymer may be varied as desired, but will generally be in an average molecular weight range from 500Da to 50000Da, preferably from 5000 to 40000Da and more preferably from 25000 to 40000Da. The polymer size may in particular be selected on the basis of the intended use of the product. Thus, for example, where the product is intended to leave the circulation and penetrate tissue, for example for use in the treatment of a tumour, it may be advantageous to use a small molecular weight polymer, for example with a molecular weight of around 5000Da. For applications where the product remains in the circulation, it may be advantageous to use a higher molecular weight polymer, for example having a molecular weight in the range from 25000Da to 40000Da.

Particularly preferred polymers include a polyalkylene polymer, such as a poly(ethyleneglycol) or, especially, a methoxypoly(ethyleneglycol) or a derivative thereof, and especially with a molecular weight in the range from about 25000Da to about 40000Da.

Each polymer molecule attached to the modified antibody fragment may be covalently linked to the sulphur atom of a cysteine residue located in the fragment. The covalent linkage will generally be a disulphide bond or, in particular, a sulphur-carbon bond.

Where desired, the antibody fragment may have one or more effector or reporter molecules attached to it. The effector or reporter molecules may be attached to the antibody fragment through any available amino acid side-chain or terminal amino acid functional group located in the fragment, for example any free amino, imino, hydroxyl or carboxyl group.

An activated polymer may be used as the starting material in the preparation of polymer-modified antibody fragments as described above. The activated polymer may be any polymer containing a thiol reactive group such as an α-halocarboxylic acid or ester, e.g. iodoacetamide, an imide, e.g. maleimide, a vinyl sulphone or a disulphide. Such starting materials may be obtained commercially (for example from Nektar Therapeutics, Inc (Huntsville, AL) or may be prepared from commercially available starting materials using conventional chemical procedures.

Standard chemical or recombinant DNA procedures in which the antibody fragment is linked either directly or via a coupling agent to the effector or reporter molecule either before or after reaction with the activated polymer as appropriate may be used. Particular chemical procedures include, for example, those described in WO 93/06231, WO 92/22583, WO 90/09195, WO 89/01476, WO 99/15549 and WO 03/031581. Alternatively, where the effector or reporter molecule is a protein or polypeptide the linkage may be achieved using recombinant DNA procedures, for example as described in WO 86/01533 and EP 0392745.

Most preferably antibodies are attached to poly(ethyleneglycol) (PEG) moieties. Preferably, a modified Fab fragment is PEGylated, *i.e.* has PEG (poly(ethyleneglycol)) covalently attached thereto, *e.g.* according to the method disclosed in EP 0948544 [see also "Poly(ethyleneglycol) Chemistry, Biotechnical and Biomedical Applications", 1992, J. Milton Harris (ed), Plenum Press, New York; "Poly(ethyleneglycol) Chemistry and Biological Applications", 1997, J. Milton Harris and S. Zalipsky (eds), American Chemical Society, Washington DC and "Bioconjugation Protein Coupling Techniques for the Biomedical Sciences", 1998, M. Aslam and A. Dent, Grove Publishers, New York; Chapman, A. 2002, Advanced Drug Delivery Reviews 2002, 54:531-545]. In one embodiment, a PEG modified Fab fragment has a maleimide group covalently linked to a single thiol group in a modified hinge region. A lysine residue may be covalently linked to the maleimide group. To each of the amine groups on the lysine residue may be attached a methoxypoly(ethyleneglycol) polymer having a molecular weight of approximately 20,000 Da. The total molecular weight of the entire effector molecule may therefore be approximately 40,000 Da.

MAL2 polypeptides or cells expressing said polypeptides can be used to produce antibodies, *e.g.* which interact with or recognise said MAL2 polypeptides. Antibodies

generated against a MAL2 polypeptide may be obtained by administering the polypeptides to an animal, preferably a non-human animal, using well-known and routine protocols.

Anti-MAL2 antibodies include functionally active fragments, derivatives or analogues and may be, but are not limited to, polyclonal, monoclonal, bi-, tri- or tetra-valent antibodies, humanized or chimeric antibodies, single chain antibodies, Fab fragments, Fab' and Fab'$_2$ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule (see, *e.g.* US 5,585,089). Antibodies include immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.* molecules that contain an antigen binding site that specifically binds an antigen. The immunoglobulin molecules of the invention can be of any class (*e.g.* IgG, IgE, IgM, IgD and IgA) or subclass of immunoglobulin molecule.

Monoclonal antibodies may be prepared by any method known in the art such as the hybridoma technique (Kohler & Milstein, 1975, Nature, 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.,* 1983, Immunology Today, 4:72) and the EBV-hybridoma technique (Cole *et al.,* Monoclonal Antibodies and Cancer Therapy, pp77-96, Alan R Liss, Inc., 1985).

Chimeric antibodies are those antibodies encoded by immunoglobulin genes that have been genetically engineered so that the light and heavy chain genes are composed of immunoglobulin gene segments belonging to different species. These chimeric antibodies are likely to be less antigenic. Bivalent antibodies may be made by methods known in the art (Milstein *et al.*, 1983, Nature 305:537-539; WO 93/08829, Traunecker *et al.*, 1991, EMBO J. 10:3655-3659). Bi-, tri- and tetra-valent antibodies may comprise multiple specificities or may be monospecific (see for example WO 92/22853).

The antibodies for use in the invention may be generated using single lymphocyte antibody methods based on the molecular cloning and expression of immunoglobulin variable region cDNAs generated from single lymphocytes that were selected for the production of specific antibodies such as described by Babcook, J. *et al.*, 1996, Proc. Natl. Acad. Sci. USA 93(15):7843-7848 and in WO 92/02551.

The antibodies for use in the present invention can also be generated using various phage display methods known in the art and include those disclosed by Brinkman *et al.* (in J. Immunol. Methods, 1995, 182: 41-50), Ames *et al.* (J. Immunol. Methods, 1995, 184:177-

186), Kettleborough *et al.* (Eur. J. Immunol. 1994, 24:952-958), Persic *et al.* (Gene, 1997 187 9-18), Burton *et al.* (Advances in Immunology, 1994, 57:191-280) and WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and US 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108. Techniques for the production of single chain antibodies, such as those described in US 4,946,778 can also be adapted to produce single chain antibodies to MAL2 polypeptides. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

MAL2 polypeptides can be used for the identification of agents for use in the methods of treatment and/or prophylaxis according to the invention.

A further aspect of the invention provides methods of screening for anti-carcinoma agents that interact with a MAL2 polypeptide comprising:

(a) contacting said polypeptide with a candidate agent; and
(b) determining whether or not the candidate agent interacts with said polypeptide.

Preferably, the determination of an interaction between the candidate agent and MAL2 polypeptide comprises quantitatively detecting binding of the candidate agent and said polypeptide.

Further provided is a method of screening for anti-carcinoma agents that modulate the expression or activity of a MAL2 polypeptide comprising:

(i) comparing the expression or activity of said polypeptide in the presence of a candidate agent with the expression or activity of said polypeptide in the absence of the candidate agent or in the presence of a control agent; and
(ii) determining whether the candidate agent causes the expression or activity of said polypeptide to change.

Preferably, the expression and/or activity of a MAL2 polypeptide is compared with a predetermined reference range or control.

More preferably the method further comprises selecting an agent, which interacts with a MAL2 polypeptide or is capable of modulating the interaction, expression or activity of a MAL2 polypeptide, for further testing for use in the treatment and/or prophylaxis of carcinoma. It will be apparent to one skilled in the art that the above screening methods are also appropriate for screening for anti-carcinoma agents which interact with or modulate the expression or activity of a MAL2 nucleic acid molecule.

The invention also provides assays for use in drug discovery in order to identify or verify the efficacy of agents for treatment and/or prophylaxis of carcinoma. Agents identified

using these methods can be used as lead agents for drug discovery, or used therapeutically. Expression of a MAL2 polypeptide can be assayed by, for example, immunoassays, gel electrophoresis followed by visualisation, detection of mRNA or MAL2 polypeptide activity, or any other method taught herein or known to those skilled in the art. Such assays can be used to screen candidate agents, in clinical monitoring or in drug development.

Agents can be selected from a wide variety of candidate agents. Examples of candidate agents include but are not limited to, nucleic acids (*e.g.* DNA and RNA), carbohydrates, lipids, proteins, polypeptides, peptides, peptidomimetics, small molecules and other drugs. Agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is suited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, Anticancer Drug Des. 12:145; U.S. 5,738,996; and U.S. 5,807,683).

Examples of suitable methods based on the present description for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.*, 1993, Proc. Natl. Acad. Sci. USA 90:6909; Erb *et al.*, 1994, Proc. Natl. Acad. Sci. USA 91:11422; Zuckermann *et al.*, 1994, J. Med. Chem. 37:2678; Cho *et al.*, 1993, Science 261:1303; Carrell *et al.*, 1994, Angew. Chem. Int. Ed. Engl. 33:2059; Carell *et al.*, 1994, Angew. Chem. Int. Ed. Engl. 33:2061; and Gallop *et al.*, 1994, J. Med. Chem. 37:1233.

Libraries of compounds may be presented, for example, in solution (*e.g.* Houghten, 1992, Bio/Techniques 13:412-421), or on beads (Lam, 1991, Nature 354:82-84), chips (Fodor, 1993, Nature 364:555-556), bacteria (US 5,223,409), spores (US 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89:1865-1869) or phage (Scott and Smith, 1990, Science 249:386-390; Devlin, 1990, Science 249:404-406; Cwirla *et a.*, 1990, Proc. Natl. Acad. Sci. USA 87:6378-6382; and Felici, 1991, J. Mol. Biol. 222:301-310).

In one embodiment, agents that interact with (*e.g.* bind to) a MAL2 polypeptide are identified in a cell-based assay where a population of cells expressing a MAL2 polypeptide is contacted with a candidate agent and the ability of the candidate agent to interact with the polypeptide is determined. Preferably, the ability of a candidate agent to interact with a MAL2 polypeptide is compared to a reference range or control. In another embodiment, a first and

second population of cells expressing a MAL2 polypeptide are contacted with a candidate agent or a control agent and the ability of the candidate agent to interact with the polypeptide is determined by comparing the difference in interaction between the candidate agent and control agent. If desired, this type of assay may be used to screen a plurality (*e.g.* a library) of candidate agents using a plurality of cell populations expressing a MAL2 polypeptide. If desired, this assay may be used to screen a plurality (*e.g.* a library) of candidate agents. The cell, for example, can be of prokaryotic origin (*e.g. E. coli*) or eukaryotic origin (*e.g.* yeast or mammalian). Further, the cells can express the MAL2 polypeptide endogenously or be genetically engineered to express the polypeptide. In some embodiments, a MAL2 polypeptide or the candidate agent is labelled, for example with a radioactive label (such as ^{32}P, ^{35}S or ^{125}I) or a fluorescent label (such as fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde or fluorescamine) to enable detection of an interaction between a polypeptide and a candidate agent.

In another embodiment, agents that interact with (*e.g.* bind to) a MAL2 polypeptide are identified in a cell-free assay system where a sample expressing a MAL2 polypeptide is contacted with a candidate agent and the ability of the candidate agent to interact with the polypeptide is determined. Preferably, the ability of a candidate agent to interact with a MAL2 polypeptide is compared to a reference range or control. In a preferred embodiment, a first and second sample comprising native or recombinant MAL2 polypeptide are contacted with a candidate agent or a control agent and the ability of the candidate agent to interact with the polypeptide is determined by comparing the difference in interaction between the candidate agent and control agent. If desired, this assay may be used to screen a plurality (*e.g.* a library) of candidate agents using a plurality of MAL2 polypeptide samples. Preferably, the polypeptide is first immobilized, by, for example, contacting the polypeptide with an immobilized antibody which specifically recognizes and binds it, or by contacting a purified preparation of polypeptide with a surface designed to bind proteins. The polypeptide may be partially or completely purified (*e.g.* partially or completely free of other polypeptides) or part of a cell lysate. Further, the polypeptide may be a fusion protein comprising the MAL2 polypeptide or a biologically active portion thereof and a domain such as glutathionine-S-transferase. Alternatively, the polypeptide can be biotinylated using techniques well known to those of skill in the art (*e.g.* biotinylation kit, Pierce Chemicals; Rockford, IL). The ability of the candidate agent to interact with the polypeptide can be duplicated by methods known to those of skill in the art.

In one embodiment, a MAL2 polypeptide is used as a "bait protein" in a two-hybrid assay or three hybrid assay to identify other proteins that bind to or interact with the MAL2 polypeptide (see *e.g.* US 5,283,317; Zervos *et al.*, 1993, Cell 72:223-232; Madura *et al.* 1993, J. Biol. Chem. 268:12046-12054; Bartel *et al.*, 1993, Bio/Techniques 14:920-924; Iwabuchi *et al.*, 1993, Oncogene 8:1693-1696; and WO 94/10300). As those skilled in the art will appreciate, such binding proteins are also likely to be involved in the propagation of signals by a MAL2 polypeptide. For example, they may be upstream or downstream elements of a signalling pathway involving a MAL2 polypeptide. Alternatively, polypeptides that interact with a MAL2 polypeptide can be identified by isolating a protein complex comprising a MAL2 polypeptide (*i.e.* a MAL2 polypeptide which interacts directly or indirectly with one or more other polypeptides) and identifying the associated proteins using methods known in the art such as mass spectrometry or Western blotting (for examples see Blackstock, W. & Weir, M. 1999, Trends in Biotechnology, 17: 121-127; Rigaut, G. 1999, Nature Biotechnology, 17: 1030-1032; Husi, H. 2000, Nature Neurosci. 3:661-669; Ho, Y. *et al.*, 2002, Nature, 415:180-183; Gavin, A. *et al.*, 2002, Nature, 415: 141-147).

In all cases, the ability of the candidate agent to interact directly or indirectly with the MAL2 polypeptide can be determined by methods known to those of skill in the art. For example but without limitation, the interaction between a candidate agent and a MAL2 polypeptide can be determined by flow cytometry, a scintillation assay, an activity assay, mass spectrometry, microscopy, immunoprecipitation or western blot analysis.

In yet another embodiment, agents that competitively interact with (*i.e.* competitively binding to) a MAL2 polypeptide are identified in a competitive binding assay and the ability of the candidate agent to interact with the MAL2 polypeptide is determined. Preferably, the ability of a candidate agent to interact with a MAL2 polypeptide is compared to a reference range or control. In a preferred embodiment, a first and second population of cells expressing both a MAL2 polypeptide and a protein which is known to interact with the MAL2 polypeptide are contacted with a candidate agent or a control agent. The ability of the candidate agent to competitively interact with the MAL2 polypeptide is then determined by comparing the interaction in the first and second population of cells. In another embodiment, an alternative second population or a further population of cells may be contacted with an agent which is known to competitively interact with a MAL2 polypeptide. Alternatively, agents that competitively interact with a MAL2 polypeptide are identified in a cell-free assay system by contacting a first and second sample comprising a MAL2 polypeptide and a protein known to interact with the MAL2 polypeptide with a candidate agent or a control agent. The

ability of the candidate agent to competitively interact with the MAL2 polypeptide is then determined by comparing the interaction in the first and second sample. In another embodiment, an alternative second sample or a further sample comprising a MAL2 polypeptide may be contacted with an agent which is known to competitively interact with a MAL2 polypeptide. In any case, the MAL2 polypeptide and known interacting protein may be expressed naturally or may be recombinantly expressed; the candidate agent may be added exogenously, or be expressed naturally or recombinantly.

In another embodiment, agents that modulate the interaction between a MAL2 polypeptide and another agent, for example but without limitation a protein, may be identified in a cell-based assay by contacting cells expressing a MAL2 polypeptide in the presence of a known interacting agent and a candidate modulating agent and selecting the candidate agent which modulates the interaction. Alternatively, agents that modulate an interaction between a MAL2 polypeptide and another agent, for example but without limitation a protein, may be identified in a cell-free assay system by contacting the polypeptide with an agent known to interact with the polypeptide in the presence of a candidate agent. A modulating agent can act as an antibody, a cofactor, an inhibitor, an activator or have an antagonistic or agonistic effect on the interaction between a MAL2 polypeptide and a known agent. As stated above the ability of the known agent to interact with a MAL2 polypeptide can be determined by methods known in the art. These assays, whether cell-based or cell-free, can be used to screen a plurality (*e.g.* a library) of candidate agents.

In another embodiment, a cell-based assay system is used to identify agents capable of modulating (*i.e.* stimulating or inhibiting) the activity of a MAL2 polypeptide. Accordingly, the activity of a MAL2 polypeptide is measured in a population of cells that naturally or recombinantly express a MAL2 polypeptide, in the presence of a candidate agent. Preferably, the activity of a MAL2 polypeptide is compared to a reference range or control. In a preferred embodiment, the activity of a MAL2 polypeptide is measured in a first and second population of cells that naturally or recombinantly express a MAL2 polypeptide, in the presence of agent or absence of a candidate agent (*e.g.* in the presence of a control agent) and the activity of the MAL2 polypeptide is compared. The candidate agent can then be identified as a modulator of the activity of a MAL2 polypeptide based on this comparison. Alternatively, the activity of a MAL2 polypeptide can be measured in a cell-free assay system where the MAL2 polypeptide is either natural or recombinant. Preferably, the activity of a MAL2 polypeptide is compared to a reference range or control. In a preferred embodiment, the activity of a MAL2 polypeptide is measured in a first and second sample in the presence

or absence of a candidate agent and the activity of the MAL2 polypeptide is compared. The candidate agent can then be identified as a modulator of the activity of a MAL2 polypeptide based on this comparison.

The activity of a MAL2 polypeptide can be assessed by detecting its effect on a downstream effector, for example but without limitation, the level or activity of a second messenger (*e.g.* cAMP, intracellular Ca^{2+}, diacylglycerol, IP_3, etc.), detecting catalytic or enzymatic activity, detecting the induction of a reporter gene (*e.g.* luciferase) or detecting a cellular response, for example, proliferation, differentiation or transformation where appropriate as known by those skilled in the art (for activity measurement techniques see, *e.g.* US 5,401,639). The candidate agent can then be identified as a modulator of the activity of a MAL2 polypeptide by comparing the effects of the candidate agent to the control agent. Suitable control agents include PBS or normal saline.

In another embodiment, agents such as an enzyme, or a biologically active portion thereof, which is responsible for the production or degradation of a MAL2 polypeptide or is responsible for the post-translational modification of a MAL2 polypeptide can be identified. In a primary screen, substantially pure, native or recombinantly expressed MAL2 polypeptides, nucleic acids or cellular extract or other sample comprising native or recombinantly expressed MAL2 polypeptides or nucleic acids are contacted with a plurality of candidate agents (for example but without limitation, a plurality of agents presented as a library) that may be responsible for the processing of a MAL2 polypeptide or nucleic acid, in order to identify such agents. The ability of the candidate agent to modulate the production, degradation or post-translational modification of a MAL2 polypeptide or nucleic acid can be determined by methods known to those of skill in the art, including without limitation, flow cytometry, radiolabelling, a kinase assay, a phosphatase assay, immunoprecipitation and Western blot analysis, or Northern blot analysis.

In yet another embodiment, cells expressing a MAL2 polypeptide are contacted with a plurality of candidate agents. The ability of such an agent to modulate the production, degradation or post-translational modification of a MAL2 polypeptide can be determined by methods known to those of skill in the art, as described above.

In one embodiment, agents that modulate the expression of a MAL2 polypeptide (*e.g.* down-regulate) are identified in a cell-based assay system. Accordingly, a population of cells expressing a MAL2 polypeptide or nucleic acid are contacted with a candidate agent and the ability of the candidate agent to alter expression of the MAL2 polypeptide or nucleic acid is determined by comparison to a reference range or control. In another embodiment, a first and

second population of cells expressing a MAL2 polypeptide are contacted with a candidate agent or a control agent and the ability of the candidate agent to alter the expression of the MAL2 polypeptide or nucleic acid is determined by comparing the difference in the level of expression of the MAL2 polypeptide or nucleic acid between the first and second populations of cells. In a further embodiment, the expression of the MAL2 polypeptide or nucleic acid in the first population may be further compared to a reference range or control. If desired, this assay may be used to screen a plurality (e.g. a library) of candidate agents. The cell, for example, can be of prokaryotic origin (*e.g. E. coli*) or eukaryotic origin (*e.g.* yeast or mammalian). Further, the cells can express a MAL2 polypeptide or nucleic acid endogenously or be genetically engineered to express a MAL2 polypeptide or nucleic acid. The ability of the candidate agents to alter the expression of a MAL2 polypeptide or nucleic acid can be determined by methods known to those of skill in the art, for example and without limitation, by flow cytometry, radiolabelling, a scintillation assay, immunoprecipitation, Western blot analysis or Northern blot analysis.

In another embodiment, agents that modulate the expression of a MAL2 polypeptide or nucleic acid are identified in an animal model. Examples of suitable animals include, but are not limited to, mice, rats, rabbits, monkeys, guinea pigs, dogs and cats. Preferably, the animal used represents a model of carcinoma, for example breast cancer, colon cancer, stomach cancer or liver cancer. Accordingly, a first and second group of mammals are administered with a candidate agent or a control agent and the ability of the candidate agent to modulate the expression of the MAL2 polypeptide or nucleic acid is determined by comparing the difference in the level of expression between the first and second group of mammals. Where desired, the expression levels of the MAL2 polypeptides or nucleic acid in the first and second groups of mammals can be compared to the level of a MAL2 polypeptide or nucleic acid in a control group of mammals. The candidate agent or a control agent can be administered by means known in the art (*e.g.* orally, rectally or parenterally such as intraperitoneally or intravenously). Changes in the expression of a polypeptide or nucleic acid can be assessed by the methods outlined above. In a particular embodiment, a therapeutically effective amount of an agent can be determined by monitoring an amelioration or improvement in disease symptoms, to delay onset or slow progression of the disease, for example but without limitation, a reduction in tumour size. Techniques known to physicians familiar with carcinoma can be used to determine whether a candidate agent has altered one or more symptoms associated with the disease.

One skilled in the art will also appreciate that a MAL2 polypeptide may also be used in a method for the structure-based design of an agent, in particular a small molecule which acts to modulate (*e.g.* stimulate or inhibit) the activity of said polypeptide, said method comprising:

1) determining the three-dimensional structure of said polypeptide;
2) deducing the three-dimensional structure within the polypeptide of the likely reactive or binding site(s) of the agent;
3) synthesising candidate agents that are predicted to react or bind to the deduced reactive or binding site; and
4) testing whether the candidate agent is able to modulate the activity of said polypeptide.

It will be appreciated that the method described above is likely to be an iterative process.

As discussed herein, agents which interact with a MAL2 polypeptide find use in the treatment and/or prophylaxis of carcinoma. For such use the agents will generally be administered in the form of a pharmaceutical composition.

Thus, according to the invention there is provided a pharmaceutical composition comprising an agent which interacts with a MAL2 polypeptide and a pharmaceutically acceptable diluent, excipient and /or carrier. Pharmaceutical compositions may also find use as a vaccine and may comprise additional components acceptable for vaccine use and may additionally comprise one or more suitable adjuvants as known to the skilled person.

Hereinafter, the agents of use in the invention, MAL2 polypeptides and MAL2 nucleic acids of use in treatment and/or prophylaxis are referred to as 'active agents'. When a reference is made herein to a method of treating or preventing a disease or condition using a particular active agent or combination of agents, it is to be understood that such a reference is intended to include the use of that active agent or combination of agents in the preparation of a medicament for the treatment and/or prophylaxis of the disease or condition.

The composition will usually be supplied as part of a sterile, pharmaceutical composition that will normally include a pharmaceutically acceptable carrier. This composition may be in any suitable form (depending upon the desired method of administering it to a patient).

Active agents of the invention may be administered to a subject by any of the routes conventionally used for drug administration, for example they may be administered parenterally, orally, topically (including buccal, sublingual or transdermal) or by inhalation. The most suitable route for administration in any given case will depend on the particular

active agent, the carcinoma involved, the subject, and the nature and severity of the disease and the physical condition of the subject.

The active agents may be administered in combination, *e.g.* simultaneously, sequentially or separately, with one or more other therapeutically active, *e.g.* anti-tumour, compounds.

Pharmaceutical compositions may be conveniently presented in unit dose forms containing a predetermined amount of an active agent of the invention per dose. Such a unit may contain for example but without limitation, 750mg/kg to 0.1mg/kg depending on the condition being treated, the route of administration and the age, weight and condition of the subject.

Pharmaceutically acceptable carriers for use in the invention may take a wide variety of forms depending, *e.g.* on the route of administration.

Compositions for oral administration may be liquid or solid. Oral liquid preparations may be in the form of, for example, aqueous or oily suspensions, solutions, emulsions, syrups or elixirs, or may be presented as a dry product for reconstitution with water or other suitable vehicle before use. Oral liquid preparations may contain suspending agents as known in the art.

In the case of oral solid preparations such as powders, capsules and tablets, carriers such as starches, sugars, microcrystalline cellulose, diluents, granulating agents, lubricants, binders, disintegrating agents, and the like may be included. Because of their ease of administration, tablets and capsules represent the most advantageous oral dosage unit form in which case solid pharmaceutical carriers are generally employed. In addition to the common dosage forms set out above, active agents of the invention may also be administered by controlled release means and/or delivery devices. Tablets and capsules may comprise conventional carriers or excipients such as binding agents for example, syrup, acacia, gelatin, sorbitol, tragacanth, or polyvinylpyrrolidone; fillers, for example lactose, sugar, maize-starch, calcium phosphate, sorbitol or glycine; tableting lubricants, for example magnesium stearate, talc, polyethylene glycol or silica; disintegrants, for example potato starch; or acceptable wetting agents such as sodium lauryl sulphate. The tablets may be coated by standard aqueous or non-aqueous techniques according to methods well known in normal pharmaceutical practice.

Pharmaceutical compositions of the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets, each containing a predetermined amount of the active agent, as a powder or granules, or as a solution or a suspension in an aqueous liquid, a non-aqueous liquid, an oil-in-water emulsion or a water-in-

oil liquid emulsion. Such compositions may be prepared by any of the methods of pharmacy but all methods include the step of bringing into association the active agent with the carrier, which constitutes one or more necessary ingredients. In general, the compositions are prepared by uniformly and intimately admixing the active agent with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product into the desired presentation. For example, a tablet may be prepared by compression or moulding, optionally with one or more accessory ingredients.

Pharmaceutical compositions suitable for parenteral administration may be prepared as solutions or suspensions of the active agents of the invention in water suitably mixed with a surfactant such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include aqueous or non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the composition isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. Extemporaneous injection solutions, dispersions and suspensions may be prepared from sterile powders, granules and tablets.

Pharmaceutical compositions can be administered with medical devices known in the art. For example, in a preferred embodiment, a pharmaceutical composition of the invention can be administered with a needleless hypodermic injection device, such as the devices disclosed in US 5,399,163; 5,383,851; 5,312,335; 5,064,413; 4,941,880; 4,790,824; or 4,596,556. Examples of well-known implants and modules useful in the present invention include: US 4,487,603, which discloses an implantable micro-infusion pump for dispensing medication at a controlled rate; US 4,486,194, which discloses a therapeutic device for administering medicaments through the skin; US 4,447,233, which discloses a medication infusion pump for delivering medication at a precise infusion rate; US 4,447,224, which discloses a variable flow implantable infusion apparatus for continuous drug delivery; US 4,439,196, which discloses an osmotic drug delivery system having multi-chamber compartments; and US 4,475,196, which discloses an osmotic drug delivery system. Many other such implants, delivery systems, and modules are known to those skilled in the art.

In certain embodiments, the pharmaceutical compositions of the invention can be formulated to ensure proper distribution *in vivo*. For example, the blood-brain barrier

excludes many highly hydrophilic compounds and it may be preferable to deliver pharmaceutical compositions in liposomes. Thus, in one embodiment of the invention, the active agents of the invention are formulated in liposomes; in a more preferred embodiment, the liposomes include a targeting moiety. In a most preferred embodiment, the therapeutic compounds in the liposomes are delivered by bolus injection to a site proximal to the tumour. For methods of manufacturing liposomes, see, *e.g.* US 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties which are selectively transported into specific cells or organs, thus enhancing targeted drug delivery (*see, e.g.* Ranade, VV. 1989, J. Clin. Pharmacol. 29:685). Exemplary targeting moieties include folate or biotin (see, *e.g.* U.S. Patent 5,416,016.); mannosides (Umezawa *et al.*, 1988, Biochem. Biophys. Res. Commun. 153:1038); antibodies (Bloeman, PG. *et al.*, 1995, FEBS Lett. 357:140; M. Owais *et al.*, 1995, Antimicrob. Agents Chemother. 39:180); surfactant protein A receptor (Briscoe *et al.*, 1995, Am. J. Physiol. 1233:134), different species of which may comprise the formulations of the inventions, as well as components of the invented molecules; p120 (Schreier *et al.*, 1994, J. Biol. Chem. 269:9090); see also Keinanen, K. & Laukkanen, ML. 1994, FEBS Lett. 346:123; Killion, JJ. & Fidler, IJ. 1994, Immunomethods 4:273. The compositions may be presented in unit-dose or multi-dose containers, for example in sealed ampoules and vials and to enhance stability, may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example water for injections, immediately prior to use. The sterile liquid carrier may be supplied in a separate vial or ampoule and can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.* glycerol, propylene glycol and liquid polyethylene glycol), suitable mixtures thereof, and vegetable oils. Advantageously, agents such as a local anaesthetic, preservative and buffering agents can be included in the sterile liquid carrier.

Pharmaceutical compositions adapted for topical administration may be formulated as ointments, creams, suspensions, lotions, powders, solutions, pastes, gels, impregnated dressings, sprays, aerosols or oils, transdermal devices, dusting powders, and the like. These compositions may be prepared via conventional methods containing the active agent. Thus, they may also comprise compatible conventional carriers and additives, such as preservatives, solvents to assist drug penetration, emollients in creams or ointments and ethanol or oleyl alcohol for lotions. Such carriers may be present as from about 1% up to about 98% of the composition. More usually they will form up to about 80% of the composition. As an illustration only, a cream or ointment is prepared by mixing sufficient quantities of

hydrophilic material and water, containing from about 5-10% by weight of the compound, in sufficient quantities to produce a cream or ointment having the desired consistency.

Pharmaceutical compositions adapted for transdermal administration may be presented as discrete patches intended to remain in intimate contact with the epidermis of the recipient for a prolonged period of time. For example, the active agent may be delivered from the patch by iontophoresis.

For applications to external tissues, for example the mouth and skin, the compositions are preferably applied as a topical ointment or cream. When formulated in an ointment, the active agent may be employed with either a paraffinic or a water-miscible ointment base. Alternatively, the active agent may be formulated in a cream with an oil-in-water cream base or a water-in-oil base.

Pharmaceutical compositions adapted for topical administration in the mouth include lozenges, pastilles and mouth washes.

Pharmaceutical compositions adapted for topical administration to the eye include eye drops wherein the active agent is dissolved or suspended in a suitable carrier, especially an aqueous solvent. They also include topical ointments or creams as above.

Pharmaceutical compositions suitable for rectal administration wherein the carrier is a solid are most preferably presented as unit dose suppositories. Suitable carriers include cocoa butter or other glyceride or materials commonly used in the art, and the suppositories may be conveniently formed by admixture of the combination with the softened or melted carrier(s) followed by chilling and shaping moulds. They may also be administered as enemas.

Pharmaceutical compositions adapted for vaginal administration may be presented as pessaries, tampons, creams, gels, pastes, foams or spray compositions. These may comprise emollients or bases as commonly used in the art.

The dosage to be administered of an active agent will vary according to the particular active agent, the carcinoma involved, the subject, and the nature and severity of the disease and the physical condition of the subject, and the selected route of administration; the appropriate dosage can be readily determined by a person skilled in the art. For the treatment and/or prophylaxis of carcinoma in humans and animals pharmaceutical compositions comprising antibodies can be administered to patients (*e.g.*, human subjects) at therapeutically or prophylactically effective dosages (*e.g.* dosages which result in tumour growth inhibition and/or tumour cell migration inhibition) using any suitable route of administration, such as injection and other routes of administration known in the art for antibody-based clinical products.

The compositions may contain from 0.1% by weight, preferably from 10-60%, or more, by weight, of the active agent of the invention, depending on the method of administration.

It will be recognized by one of skill in the art that the optimal quantity and spacing of individual dosages of an active agent of the invention will be determined by the nature and extent of the condition being treated, the form, route and site of administration, and the age and condition of the particular subject being treated, and that a physician will ultimately determine appropriate dosages to be used. This dosage may be repeated as often as appropriate. If side effects develop the amount and/or frequency of the dosage can be altered or reduced, in accordance with normal clinical practice.

MAL2 polypeptides may also be of use in the treatment and/or prophylaxis of carcinoma. Accordingly, provided is a method for the treatment and/or prophylaxis of carcinoma comprising administering a therapeutically effective amount of a composition comprising a MAL2 polypeptide, preferably as a vaccine. Also provided is the use of a MAL2 polypeptide for the manufacture of a medicament for the treatment and/or prophylaxis of carcinoma. Where they are provided for use with the methods of the invention, MAL2 polypeptides are preferably provided in isolated form. More preferably the MAL2 polypeptides have been purified to at least some extent. MAL2 polypeptides can also be produced using recombinant methods, synthetically produced or produced by a combination of these methods. MAL2 polypeptides may be provided in substantially pure form, that is to say free, to a substantial extent, from other proteins.

Recombinant MAL2 polypeptides may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, the present invention also relates to expression systems which comprise a MAL2 polypeptide or MAL2 nucleic acid, to host cells which are genetically engineered with such expression systems and to the production of MAL2 polypeptides by recombinant techniques. Cell-free translation systems can also be employed to produce recombinant polypeptides (*e.g.* rabbit reticulocyte lysate, wheat germ lysate, SP6/T7 *in vitro* T&T and RTS 100 *E. Coli* HY transcription and translation kits from Roche Diagnostics Ltd., Lewes, UK and the TNT Quick coupled Transcription/Translation System from Promega UK, Southampton, UK.

For recombinant MAL2 polypeptide production, host cells can be genetically engineered to incorporate expression systems or portions thereof for MAL2 nucleic acids. Such incorporation can be performed using methods well known in the art, such as, calcium phosphate transfection, DEAD-dextran mediated transfection, transvection, microinjection,

cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection (see *e.g.* Davis *et al.*, Basic Methods in Molecular Biology, 1986 and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbour laboratory Press, Cold Spring Harbour, NY, 1989).

Representative examples of host cells include bacterial cells *e.g. E. Coli*, *Streptococci*, *Staphylococci*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, HEK 293, BHK and Bowes melanoma cells; and plant cells.

A wide variety of expression systems can be used, such as and without limitation, chromosomal, episomal and virus-derived systems, *e.g.* vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector which is able to maintain, propagate or express a nucleic acid to produce a polypeptide in a host may be used. The appropriate nucleic acid sequence may be inserted into an expression system by any variety of well-known and routine techniques, such as those set forth in Sambrook *et al., supra*. Appropriate secretion signals may be incorporated into the MAL2 polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the MAL2 polypeptide or they may be heterologous signals.

If a MAL2 polypeptide is to be expressed for use in cell-based screening assays, it is preferred that the polypeptide be produced at the cell surface. In this event, the cells may be harvested prior to use in the screening assay. If the MAL2 polypeptide is secreted into the medium, the medium can be recovered in order to isolate said polypeptide. If produced intracellularly, the cells must first be lysed before the MAL2 polypeptide is recovered.

MAL2 polypeptides can be recovered and purified from recombinant cell cultures or from other biological sources by well-known methods including, ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, affinity chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography, molecular sieving chromatography,

centrifugation methods, electrophoresis methods and lectin chromatography. In one embodiment, a combination of these methods is used. In another embodiment, high performance liquid chromatography is used. In a further embodiment, an antibody which specifically binds to a MAL2 polypeptide can be used to deplete a sample comprising a MAL2 polypeptide of said polypeptide or to purify said polypeptide. Techniques well-known in the art, may be used for refolding to regenerate native or active conformations of the MAL2 polypeptides when the polypeptides have been denatured during isolation and or purification. In the context of the present invention, MAL2 polypeptides can be obtained from a biological sample from any source, such as and without limitation, stomach, liver, breast, colon or other tissue.

MAL2 polypeptides may be in the form of a 'mature' protein or may be part of a larger protein such as a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, a pre-, pro- or prepro-protein sequence, or a sequence which aids in purification such as an affinity tag, for example, but without limitation, multiple histidine residues, a FLAG tag, HA tag or myc tag. An additional sequence which may provide stability during recombinant production may also be used. Such sequences may be optionally removed as required by incorporating a cleavable sequence as an additional sequence or part thereof. Thus, a MAL2 polypeptide may be fused to other moieties including other polypeptides. Such additional sequences and affinity tags are well known in the art.

Amino acid substitutions may be conservative or semi-conservative as known in the art and preferably do not significantly affect the desired activity of the polypeptide. Substitutions may be naturally occurring or may be introduced for example using mutagenesis (*e.g.* Hutchinson et al., 1978, J. Biol. Chem. 253:6551). Thus, the amino acids glycine, alanine, valine, leucine and isoleucine can often be substituted for one another (amino acids having aliphatic side chains). Of these possible substitutions, it is preferred that glycine and alanine are used to substitute for one another (since they have relatively short side chains) and that valine, leucine and isoleucine are used to substitute for one another (since they have larger aliphatic side chains which are hydrophobic). Other amino acids which can often be substituted for one another include but are not limited to:

- phenylalanine, tyrosine and tryptophan (amino acids having aromatic side chains);
- lysine, arginine and histidine (amino acids having basic side chains);
- aspartate and glutamate (amino acids having acidic side chains);
- asparagine and glutamine (amino acids having amide side chains);

- cysteine and methionine (amino acids having sulphur-containing side chains); and
- aspartic acid and glutamic acid can substitute for phospho-serine and phospho-threonine, respectively (amino acids with acidic side chains).

In one particular embodiment, the substituted amino acid(s) do significantly affect the activity of the MAL2 polypeptide and may be selected specifically to render dominant negative activity upon the peptide. In another embodiment, the substituted amino acid(s) may be selected specifically to render the polypeptide constitutively active.

Modifications include naturally occurring modifications such as and without limitation, post-translational modifications and also non-naturally occurring modifications such as may be introduced by mutagenesis.

Preferably a derivative of a MAL2 polypeptide has at least 70% identity to the amino acid sequence shown in Figure 1 (SEQ ID NO:1), more preferably it has at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% identity. Percentage identity is a well known concept in the art and can be calculated using, for example but without limitation, the BLAST™ software available from NCBI (Altschul, S.F. *et al.*, 1990, J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. 1993, Nature Genet. 3:266-272. Madden, T.L. *et al.*, 1996, Meth. Enzymol. 266:131-141; Altschul, S.F. *et al.*, 1997, Nucleic Acids Res. 25:3389-3402; Zhang, J. & Madden, T.L. 1997, Genome Res. 7:649-656).

A fragment of a MAL2 polypeptide may also be of use in the methods of the invention and includes a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:1, which has at least 70% homology over the length of the fragment. Preferably, said fragments are at least 10 amino acids in length, preferably they are at least 20, at least 30, at least 50 or at least 100 amino acids in length. A fragment has at least 70% identity over its length to the amino acid sequence shown in Figure 1 (SEQ ID NO: 1), more preferably it has at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% identity.

Where a MAL2 polypeptide is the active agent of a pharmaceutical composition for use in the treatment and/or prophylaxis of carcinoma, preferably recombinant MAL2 polypeptides are used. In a particular embodiment, a MAL2 polypeptide fused to another polypeptide, such as the protein transduction domain of the HIV/Tat protein, which facilitates the entry of the fusion protein into a cell (Asoh, S. *et al.*, 2002, Proc. Natl. Acad. Sci. USA, 99:17107-17112) is provided for use for the manufacture of a medicament for the treatment and/or prophylaxis of carcinoma.

In another aspect, detection of a MAL2 polypeptide in a subject with carcinoma may be used to identify in particular an appropriate patient population for treatment according to the methods of the invention.

Accordingly, the present invention provides a method of screening for and/or diagnosis or prognosis of carcinoma in a subject, and/or monitoring the effectiveness of carcinoma therapy, which comprises the step of detecting and/or quantifying in a biological sample obtained from said subject, the expression of a MAL2 polypeptide. The MAL2 polypeptide for use in the method of screening and/or diagnosis preferably:

(a) comprises or consists of the amino acid sequence of SEQ ID NO:1;

(b) is a derivative having one or more amino acid substitutions, modifications, deletions or insertions relative to the amino acid sequence of SEQ ID NO:1 which retains the activity of MAL2; or

(c) is a fragment of a polypeptide having the amino acid sequence of SEQ ID NO: 1, which is at least ten amino acids long and has at least 70% homology over the length of the fragment.

In one aspect, the expression is compared to a previously determined reference range. Preferably, the step of detecting comprises:

(a) contacting the sample with a capture reagent that is specific for a polypeptide as defined in (a) to (c), above; and

(b) detecting whether binding has occurred between the capture reagent and said polypeptide in the sample.

In another aspect, the captured polypeptide is detected using a directly or indirectly labelled detection reagent which may be immobilised on a solid phase.

A convenient means for detecting/quantifying a MAL2 polypeptide involves the use of antibodies. A MAL2 polypeptide can be used as an immunogen to raise antibodies which interact with (bind to or recognise) said polypeptide using methods known in the art as described above. Thus, in a further aspect, the present invention provides the use of an antibody that specifically binds to at least one MAL2 polypeptide for screening for, and/or diagnosis of, carcinoma in a subject or for monitoring the efficacy of an anti-carcinoma therapy. In a particular embodiment, the methods of diagnosis using an anti-MAL2 polypeptide antibody can be used to identify an appropriate patient population for treatment according to the methods of the invention.

MAL2 antibodies can also be used, *inter alia,* for the diagnosis of carcinoma by detecting MAL2 expression in a biological sample of human tissue and/or in subfractions thereof, for example but without limitation, membrane, cytosolic or nuclear subfractions.

In a further aspect, the method of detecting a MAL2 polypeptide in a biological sample comprises detecting and/or quantitating the expression of MAL2 polypeptide in said sample using a directly or indirectly labelled detection reagent. A MAL2 polypeptide can be detected by means of any immunoassay known in the art, including, without limitation, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis, 2 dimensional gel electrophoresis, competitive and non-competitive assay systems using techniques such as Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays and protein A immunoassays.

Detection of the interaction of an antibody with an antigen can be facilitated by coupling the antibody to a detectable substance for example, but without limitation, an enzyme (such as horseradish peroxidase, alkaline phosphatase, beta-galactosidase, acetylcholinesterase), a prosthetic group (such as streptavidin, avidin, biotin), a fluorescent material (such as umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride, phycoerythrin), a luminescent material (such as luminol), a bioluminescent material (such as luciferase, luciferin, aequorin), a radioactive nuclide (such as ^{125}I, ^{131}I, ^{111}In, ^{99}Tc) a positron emitting metal or a non-radioactive paramagnetic metal ion (see US 4,741,900).

The invention also provides diagnostic kits, comprising a capture reagent (*e.g.* an antibody) against a MAL2 polypeptide as defined above. In addition, such a kit may optionally comprise one or more of the following:

(1) instructions for using the capture reagent for screening, diagnosis, prognosis, therapeutic monitoring or any combination of these applications;

(2) a labelled binding partner to the capture reagent;

(3) a solid phase (such as a reagent strip) upon which the capture reagent is immobilised; and

(4) a label or insert indicating regulatory approval for screening, diagnostic, prognostic or therapeutic use or any combination thereof.

If no labelled binding partner to the capture reagent is provided, the anti-polypeptide capture reagent itself can be labelled with a detectable marker, *e.g.* a chemiluminescent, enzymatic, fluorescent, or radioactive moiety (see above).

It will also be apparent to one skilled in the art that detection and/or quantitation of a MAL2 nucleic acid may be used in a method of screening for and/or diagnosis or prognosis of carcinoma in a subject, and/or monitoring the effectiveness of carcinoma therapy.

Unless the context indicates otherwise, MAL2 nucleic acids include those nucleic acid molecules which may have one or more of the following characteristics and thus may:

d) comprise or consist of the DNA sequence of SEQ ID NO:3 or its RNA equivalent;
e) have a sequence which is complementary to the sequences of d);
f) have a sequence which codes for a MAL2 polypeptide;
g) have a sequence which shows substantial identity with any of those of d), e) and f); or
h) is a fragment of d), e), f) or g), which is at least 10 nucleotides in length. and may have one or more of the following characteristics:
    1) they may be DNA or RNA;
    2) they may be single or double stranded;
    3) they may be in substantially pure form. Thus, they may be provided in a form which is substantially free from contaminating proteins and/or from other nucleic acids; and
    4) they may be with introns or without introns (*e.g.* as cDNA).

Fragments of MAL2 nucleic acids are preferably at least 20, at least 30, at least 50, at least 100 or at least 250 nucleotides in length.

The invention also provides the use of nucleic acids which are complementary to the MAL2 nucleic acids described in (d)-(f) above, and can hybridise to said MAL2 nucleic acids. Such nucleic acid molecules are referred to as "hybridising" nucleic acid molecules. For example, but without limitation, hybridising nucleic acid molecules can be useful as probes or primers. Hybridising nucleic acid molecules may have a high degree of sequence identity along its length with a nucleic acid molecule within the scope of (d)-(f) above (*e.g.* at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity). The use of hybridising nucleic acid molecules that can hybridise to any of the nucleic acid molecules discussed above, *e.g.* in hybridising assays, is also covered by the present invention.

Hybridisation assays can be used for screening, prognosis, diagnosis, or monitoring of therapy of carcinoma in a subject. Accordingly, such a hybridisation assay comprises:

i) contacting a biological sample, obtained from a subject, containing nucleic acid with a nucleic acid probe capable of hybridising to a MAL2 nucleic acid molecule, under conditions such that hybridisation can occur; and

ii) detecting or measuring any resulting hybridisation.

Preferably, such hybridising molecules are at least 10 nucleotides in length and are preferably at least 25 or at least 50 nucleotides in length. More preferably, the hybridising nucleic acid molecules specifically hybridise to nucleic acids within the scope of any one of (d) to (f), above. Most preferably, the hybridisation occurs under stringent hybridisation conditions. One example of stringent hybridisation conditions is where attempted hybridisation is carried out at a temperature of from about 35°C to about 65°C using a salt solution which is about 0.9M. However, the skilled person will be able to vary such conditions as appropriate in order to take into account variables such as probe length, base composition, type of ions present, etc.

The invention also provides a diagnostic kit comprising a nucleic acid probe capable of hybridising to RNA encoding a MAL2 polypeptide, suitable reagents and instructions for use.

In a further embodiment, a diagnostic kit is provided comprising in one or more containers a pair of primers that under appropriate reaction conditions can prime amplification of at least a portion of a MAL2 nucleic acid molecule, such as by polymerase chain reaction (see *e.g.* Innis *et al.*, 1990, PCR Protocols, Academic Press, Inc., San Diego, CA), ligase chain reaction (see EP 320,308) use of Qβ replicase, cyclic probe reaction, or other methods known in the art. Typically, primers are at least eight nucleotides long and will preferably be at least ten to twenty-five nucleotides long and more preferably fifteen to twenty-five nucleotides long. In some cases, primers of at least thirty or at least thirty-five nucleotides in length may be used.

In yet another aspect, the present invention provides the use of at least one MAL2 nucleic acid for the manufacture of a medicament for use in the treatment and/or prophylaxis of carcinoma.

In a specific embodiment, hybridising MAL2 nucleic acid molecules are used as anti-sense molecules, to alter the expression of MAL2 polypeptides by binding to complementary MAL2 nucleic acids and can be used in the treatment and/or prophylaxis or prevention of carcinoma. An antisense nucleic acid includes a MAL2 nucleic acid capable of hybridising by virtue of some sequence complementarity to a portion of an RNA (preferably mRNA)

encoding a MAL2 polypeptide. The antisense nucleic acid can be complementary to a coding and/or non-coding region of an mRNA encoding such a polypeptide. Most preferably, expression of a MAL2 polypeptide is inhibited by use of antisense nucleic acids. Thus, the present invention provides the therapeutic or prophylactic use of nucleic acids comprising at least eight nucleotides that are antisense to a gene or cDNA encoding a MAL2 polypeptide.

In another embodiment, symptoms of carcinoma may be ameliorated by decreasing the level or activity of a MAL2 polypeptide by using gene sequences encoding a polypeptide as defined herein in conjunction with well-known gene "knock-out," ribozyme or triple helix methods to decrease gene expression of the polypeptide. In this approach, ribozyme or triple helix molecules are used to modulate the activity, expression or synthesis of the gene, and thus to ameliorate the symptoms of the carcinoma. Such molecules may be designed to reduce or inhibit expression of a mutant or non-mutant target gene. Techniques for the production and use of such molecules are well known to those of skill in the art.

Endogenous MAL2 polypeptide expression can also be reduced by inactivating or "knocking out" the gene encoding the polypeptide, or the promoter of such a gene, using targeted homologous recombination (*e.g.* see Smithies, *et al.*, 1985, Nature 317:230-234; Thomas & Capecchi, 1987, Cell 51:503-512; Thompson *et al.*, 1989, Cell 5:313-321; and Zijlstra *et al.*, 1989, Nature 342:435-438). For example, a mutant gene encoding a non-functional polypeptide (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous MAL2 gene (either the coding regions or regulatory regions of the gene encoding the polypeptide) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the target gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the target gene.

In another embodiment, the nucleic acid is administered via gene therapy (see for example Hoshida, T. *et al.,* 2002, Pancreas, 25:111-121; Ikuno, Y. 2002, Invest. Ophthalmol. Vis. Sci. 2002 43:2406-2411; Bollard, C., 2002, Blood 99:3179-3187; Lee E., 2001, Mol. Med. 7:773-782). Gene therapy refers to administration to a subject of an expressed or expressible MAL2 nucleic acid. Any of the methods for gene therapy available in the art can be used according to the present invention.

Delivery of the therapeutic MAL2 nucleic acid into a patient can be direct *in vivo* gene therapy (*i.e.* the patient is directly exposed to the nucleic acid or nucleic acid-containing vector) or indirect *ex vivo* gene therapy (*i.e.* cells are first transformed with the nucleic acid *in vitro* and then transplanted into the patient).

For example for *in vivo* gene therapy, an expression vector containing the MAL2 nucleic acid is administered in such a manner that it becomes intracellular; *i.e.* by infection using a defective or attenuated retroviral or other viral vectors as described, for example in US 4,980,286 or by Robbins *et al.*, 1998, Pharmacol. Ther. 80:35-47.

The various retroviral vectors that are known in the art are such as those described in Miller *et al.* (1993, Meth. Enzymol. 217:581-599) which have been modified to delete those retroviral sequences which are not required for packaging of the viral genome and subsequent integration into host cell DNA. Also adenoviral vectors can be used which are advantageous due to their ability to infect non-dividing cells and such high-capacity adenoviral vectors are described in Kochanek (1999, Human Gene Therapy, 10:2451-2459). Chimeric viral vectors that can be used are those described by Reynolds *et al.* (1999, Molecular Medicine Today, 1:25 –31). Hybrid vectors can also be used and are described by Jacoby *et al.* (1997, Gene Therapy, 4:1282-1283).

Direct injection of naked DNA or through the use of microparticle bombardment (*e.g.* Gene Gun®; Biolistic, Dupont) or by coating it with lipids can also be used in gene therapy. Cell-surface receptors/transfecting compounds or through encapsulation in liposomes, microparticles or microcapsules or by administering the nucleic acid in linkage to a peptide which is known to enter the nucleus or by administering it in linkage to a ligand predisposed to receptor-mediated endocytosis (See Wu & Wu, 1987, J. Biol. Chem., 262:4429-4432) can be used to target cell types which specifically express the receptors of interest.

In another embodiment a nucleic acid ligand compound comprising a MAL2 nucleic acid can be produced in which the ligand comprises a fusogenic viral peptide designed so as to disrupt endosomes, thus allowing the MAL2 nucleic acid to avoid subsequent lysosomal degradation. The MAL2 nucleic acid can be targeted, *in vivo,* for cell specific endocytosis and expression by targeting a specific receptor, such as that described in WO 92/06180, WO 93/14188 and WO 93/20221. Alternatively the nucleic acid can be introduced intracellularly and incorporated within the host cell genome for expression by homologous recombination (See Zijlstra et al, 1989, Nature, 342:435-428).

In *ex vivo* gene therapy, a gene is transferred into cells *in vitro* using tissue culture and the cells are delivered to the patient by various methods such as injecting subcutaneously, application of the cells into a skin graft and the intravenous injection of recombinant blood cells such as haematopoietic stem or progenitor cells.

Cells into which a MAL2 nucleic acid can be introduced for the purposes of gene therapy include, for example, epithelial cells, endothelial cells, keratinocytes, fibroblasts,

muscle cells, hepatocytes and blood cells. The blood cells that can be used include, for example, T-lymphocytes, B-lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryotcytes, granulocytes, haematopoietic cells or progenitor cells, and the like.

In one aspect, the pharmaceutical composition comprises a MAL2 nucleic acid, said nucleic acid being part of an expression vector that expresses a MAL2 polypeptide or chimeric protein thereof in a suitable host. In particular, such a nucleic acid has a promoter operably linked to the polypeptide coding region, said promoter being inducible or constitutive (and, optionally, tissue-specific). In another particular embodiment, a nucleic acid molecule is used in which the coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the nucleic acid (Koller & Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra *et al.*, 1989, Nature 342:435-438).

MAL2 nucleic acids may be obtained using standard cloning and screening techniques, from a cDNA library derived from mRNA in human cells, using expressed sequence tag (EST) analysis (Adams, M. *et al.*, 1991, Science, 252:1651-1656; Adams, M. *et al.*, 1992, Nature 355:632-634; Adams, M. *et al.*, 1995, Nature, 377:Suppl: 3-174). MAL2 nucleic acids can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques. The MAL2 nucleic acids comprising coding sequence for MAL2 polypeptides described above can be used for the recombinant production of said polypeptides. The MAL2 nucleic acids may include the coding sequence for the mature polypeptide, by itself; or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, pro- or prepro-protein sequence, a cleavable sequence or other fusion peptide portions, such as an affinity tag or an additional sequence conferring stability during production of the polypeptide. Preferred affinity tags include multiple histidine residues (for example see Gentz *et al.*, 1989, Proc. Natl. Acad. Sci USA 86:821-824), a FLAG tag, HA tag or myc tag. The MAL2 nucleic acids may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

MAL2 polypeptide derivatives, above. can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of a MAL2 nucleic acid such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Standard techniques known to those of skill in the art can be used to introduce mutations, including, for example, site-directed mutagenesis and

PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues.

A MAL2 nucleic acid encoding a MAL2 polypeptide, including homologues and orthologues from species other than human, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridisation conditions with a labelled probe having the sequence of a MAL2 nucleic acid as described in (d)-(f) above, and isolating full-length cDNA and genomic clones containing said nucleic acid sequence. Such hybridisation techniques are well-known in the art. One example of stringent hybridisation conditions is where attempted hybridisation is carried out at a temperature of from about 35°C to about 65°C using a salt solution of about 0.9M. However, the skilled person will be able to vary such conditions as appropriate in order to take into account variables such as probe length, base composition, type of ions present, etc. For a high degree of selectivity, relatively stringent conditions such as low salt or high temperature conditions, are used to form the duplexes. Highly stringent conditions include hybridisation to filter-bound DNA in 0.5M $NaHPO_4$, 7% sodium dodecyl sulphate (SDS), 1mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. *et al.*, eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, at p. 2.10.3). For some applications, less stringent conditions for duplex formation are required. Moderately stringent conditions include washing in 0.2xSSC/0.1% SDS at 42°C (Ausubel *et al.*, 1989, *supra*). Hybridisation conditions can also be rendered more stringent by the addition of increasing amounts of formamide, to destabilise the hybrid duplex. Thus, particular hybridisation conditions can be readily manipulated, and will generally be chosen as appropriate. In general, convenient hybridisation temperatures in the presence of 50% formamide are: 42°C for a probe which is 95-100% identical to the fragment of a gene encoding a polypeptide as defined herein, 37°C for 90-95% identity and 32°C for 70-90% identity.

One skilled in the art will understand that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide is cut short at the 5' end of the cDNA. This is a consequence of reverse transcriptase, an enzyme with inherently low processivity (a measure of the ability of the enzyme to remain attached to the template during the polymerization reaction), failing to complete a DNA copy of the mRNA template during 1st strand cDNA synthesis.

Methods to obtain full length cDNAs or to extend short cDNAs are well known in the art, for example RACE (Rapid amplification of cDNA ends; *e.g.* Frohman *et al.,* 1988, Proc. Natl. Acad. Sci USA 85:8998-9002). Recent modifications of the technique, exemplified by

the Marathon™ technology (Clontech Laboratories Inc.) have significantly simplified the search for longer cDNAs. This technology uses cDNAs prepared from mRNA extracted from a chosen tissue followed by the ligation of an adaptor sequence onto each end. PCR is then carried out to amplify the missing 5'-end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using nested primers which have been designed to anneal with the amplified product, typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the known gene sequence. The products of this reaction can then be analysed by DNA sequencing and a full length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full length PCR using the new sequence information for the design of the 5' primer.

A further aspect of the invention relates to a vaccine composition of use in the treatment and/or prophylaxis of carcinoma. A MAL2 polypeptide or nucleic acid as described above can be used in the production of vaccines for treatment and/or prophylaxis of carcinoma. Such material can be antigenic and/or immunogenic. Antigenic includes a protein or nucleic acid that is capable of being used to raise antibodies or indeed is capable of inducing an antibody response in a subject. Immunogenic material includes a protein or nucleic acid that is capable of eliciting an immune response in a subject. Thus, in the latter case, the protein or nucleic acid may be capable of not only generating an antibody response but, in addition, a non-antibody based immune responses, *i.e.* a cellular or humoral response. It is well known in the art that it is possible to identify those regions of an antigenic or immunogenic polypeptide that are responsible for the antigenicity or immunogenicity of said polypeptide, *i.e.* an epitope or epitopes. Amino acid and peptide characteristics well known to the skilled person can be used to predict the antigenic index (a measure of the probability that a region is antigenic) of a MAL2 polypeptide. For example, but without limitation, the 'Peptidestructure' program (Jameson and Wolf, 1988, CABIOS, 4(1):181) and a technique referred to as 'Threading' (Altuvia Y. *et al.*, 1995, J. Mol. Biol. 249:244) can be used. Thus, the MAL2 polypeptides may include one or more such epitopes or be sufficiently similar to such regions so as to retain their antigenic/immunogenic properties.

Since a polypeptide or a nucleic acid may be broken down in the stomach, the vaccine composition is preferably administered parenterally (*e.g.* subcutaneous, intramuscular, intravenous or intradermal injection).

Accordingly, in further embodiments, the present invention provides:

a) the use of such a vaccine in inducing an immune response in a subject; and

b) a method for the treatment and/or prophylaxis of carcinoma in a subject, or of vaccinating a subject against carcinoma which comprises the step of administering to the subject an effective amount of a MAL2 polypeptide or nucleic acid, preferably as a vaccine.

Preferred features of each embodiment of the invention are as for each of the other embodiments *mutatis mutandis*. All publications, including but not limited to patents and patent applications cited in this specification are herein incorporated by reference as if each individual publication were specifically and individually indicated to be incorporated by reference herein as though fully set forth.

The invention will now be described with reference to the following examples, which are merely illustrative and should not in any way be construed as limiting the scope of the present invention.

Figure 1 shows the amino acid sequence of MAL2 (Accession Nos. AAG15576.1/Q969L2); SEQ ID NO:1. The tandem mass spectrum peptide is shown in bold and underlined typeface.

Figure 2a shows the nucleic acid sequence of MAL2 (Accession No. AY007723); SEQ ID NO:2.

Figure 2b shows the cDNA sequence of MAL2; SEQ ID NO:3.

Figure 3 shows the expression of MAL2 mRNA in patient matched adjacent normal (open bars) and tumour (black bars) breast tissues and in breast cancer cell lines (hatched bars); mRNA levels were quantified by real time RT-PCR and are expressed as the number of copies ng^{-1} cDNA.

Figure 4 shows the expression of MAL2 mRNA in patient matched adjacent normal liver and colorectal tissue (open bars) and liver and colorectal tumour tissue (black bars) and in liver and colorectal tumour-derived cell lines (hatched bars); mRNA levels were quantified by real time RT-PCR and are expressed as the number of copies ng^{-1} cDNA.

Example 1 – Isolation of MAL2 Protein from Stomach, Colon and Liver Tumour-Derived Cell Lines:

Proteins in stomach and liver tumour-derived cell line membranes were separated by SDS-PAGE and analysed.

1a - Cell culture

Hepatic cancer line pool Hep 3B 2.1-7 and Hep G2 were cultured in EMEM + 2 mM Glut + 1mM NaPyr + 1%NEAA + 10% FBS and EMEM + 2 mM Glut + 1%NEAA + 10% FBS, respectively. Colon cancer cell line pool HT29 and LS174T were cultured in McCoy's + 2 mM Glut + 10% FBS and MEM + 2mM glutamine + 10% FBS + 1% NEAA, respectively. Gastric cell line pool NCI-N87, NCI-SNU-1, KATO-III and AGS were cultured in RPMI + 2 mM Glut + 10%FBS, RPMI + 2 mM Glut + 10%FBS, RPMI + 2 mM Glut + 20%FBS and Ham's F12 + 2 mM Glut + 10% FBS, respectively. The cells were grown at 37°C in a humidified atmosphere of 95% air and 5% carbon dioxide.

1b - Cell fractionation and plasma membrane generation

Purified membrane preparations were isolated from the cell lines. Adherent cells (2 x 10^8) were washed three times with PBS and scraped using a plastic cell lifter. Cells were centrifuged at 1000 x g for 5 min at 4°C and the cell pellet was resuspended in homogenisation buffer (250 mM Sucrose, 10mM HEPES, 1mM EDTA, 1mM Vanadate and 0.02% azide, protease inhibitors). Cells were fractionated using a ball bearing homogeniser (8.002 mm ball, HGM Lab equipment) until approx. 95% of cells were broken. Membranes were fractionated using the method described by Pasquali *et al* (Pasquali C. *et al.*, 1999 J. Chromatography 722: pp 89-102). The fractionated cells were centrifuged at 3000 x g for 10 min at 4°C and the postnuclear supernatant was layered onto a 60% sucrose cushion and centrifuged at 100 000 x g for 45 min. The membranes were collected using a pasteur pipette and layered on a preformed 15 to 60% sucrose gradient and spun at 100 000 x g for 17hrs. Proteins from the fractionated sucrose gradient were run on a 4-20% 1D gel (Novex) and subject to western blotting; those fractions containing alkaline phosphatase and transferrin immunoreactivity but not oxidoreductase II or calnexin immunoreactivity were pooled and represented the plasma membrane fraction.

1c - Preparation of plasma membrane fractions for 1D-gel analysis

Plasma membrane fractions that had transferrin immunoreactivity but no oxidoreductase II or calnexin immunoreactivity were identified and pooled. This pool which represented the plasma membrane fraction was diluted at least four times with 10mM HEPES, 1mM EDTA 1mM Vanadate, 0.02% Azide and added to a SW40 or SW60 tube and centrifuged at 100 000 x g for 45min with slow acceleration and deceleration. The supernatant was removed from the resulting membrane pellet and the pellet washed three times with PBS-CM. The membrane pellet was solubilised in 2% SDS in 63mM TrisHCl, pH 7.4. A protein assay was performed followed by the addition of mercaptoethanol (2% final),

glycerol (10%) and bromophenol blue (0.0025% final) was added. A final protein concentration of 1 microgram/microlitre was used for 1D-gel loading.

1d - 1D-gel technology

Protein or membrane pellets were solubilised in 1D-sample buffer (approximately 1mg/ml) and the mixture heated to 95°C for 5 min.

Samples were separated using 1D-gel electrophoresis on pre-cast 8-16% gradient gels purchased from Bio-Rad (Bio-Rad Laboratories, Hemel Hempstead, UK). A sample containing 30-50 micrograms of the protein mixtures obtained from a detergent extract were applied to the stacking gel wells using a micro-pipette. A well containing molecular weight markers (10, 15, 25, 37, 50, 75, 100, 150 and 250 kDa) was included for calibration by interpolation of the separating gel after imaging. Separation of the proteins was performed by applying a current of 30mA to the gel for approximately 5hrs or until the bromophenol blue marker dye had reached the bottom of the gel.

After electrophoresis the gel plates were prised open, the gel placed in a tray of fixer (10% acetic acid, 40% ethanol, 50% water) and shaken overnight. The gel was then primed for 30 minutes by shaking in a primer solution (7.5% acetic acid, 0.05% SDS in Milli-Q water) followed by incubation with a fluorescent dye (0.06% OGS dye in 7.5% acetic acid) with shaking for 3hrs. A preferred fluorescent dye is disclosed in US Patent No. 6,335,446. Sypro Red (Molecular Probes, Inc., Eugene, Oregon) is a suitable alternative dye for this purpose.

A digital image of the stained gel was obtained by scanning on a Storm Scanner (Molecular Dynamics Inc, USA) in the blue fluorescence mode. The captured image was used to determine the area of the gel to excise for in-gel proteolysis.

1e - Recovery and analysis of selected proteins

Each vertical lane of the gel was excised using a stainless steel scalpel blade. Proteins were processed using in-gel digestion with trypsin (Modified trypsin, Promega, Wisconsin, USA) to generate tryptic digest peptides. Recovered samples were divided into two. Prior to MALDI analysis samples were desalted and concentrated using C18 Zip Tips™ (Millipore, Bedford, MA). Samples for tandem mass spectrometry were purified using a nano LC system (LC Packings, Amsterdam, The Netherlands) incorporating C18 SPE material. Recovered peptide pools were analysed by MALDI-TOF-mass spectrometry (Voyager STR, Applied Biosystems, Framingham, MA) using a 337 nm wavelength laser for desorption and the reflectron mode of analysis. Pools were also analyzed by nano-LC tandem mass spectrometry (LC/MS/MS) using a Micromass Quadrupole Time-of-Flight (Q-TOF) mass spectrometer

(Micromass, Altrincham, UK). For partial amino acid sequencing and identification of stomach, colon and liver cancer cell membrane proteins uninterpreted tandem mass spectra of tryptic peptides were searched against a database of public domain proteins constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI) which is accessible at http://www.ncbi.nlm.nih.gov/ using the SEQUEST search program (Eng *et al.*, 1994, J. Am. Soc. Mass Spectrom. 5:976-989), version v.C.1. Criteria for database identification included: the cleavage specificity of trypsin; the detection of a suite of a, b and y ions in peptides returned from the database, and a mass increment for all Cys residues to account for carbamidomethylation. Following identification of proteins through spectral-spectral correlation using the SEQUEST program, masses detected in MALDI-TOF mass spectra were assigned to tryptic digest peptides within the proteins identified. In cases where no amino acid sequences could be identified through searching with uninterpreted MS/MS spectra of tryptic digest peptides using the SEQUEST program, tandem mass spectra of the peptides were interpreted manually, using methods known in the art. (In the case of interpretation of low-energy fragmentation mass spectra of peptide ions see Gaskell *et al.*, 1992, Rapid Commun. Mass Spectrom. 6:658-662). The method described in WO 02/21139 was also used to interpret mass spectra.

A tandem spectrum (shown in bold and underlined in Figure 1) was found to match the GenBank and SwissProt accession numbers AAG15576.1 and Q969L2, respectively in all cancer cell lines.

Example 2: Normal Tissue Distribution and Disease Tissue Upregulation of MAL2 using Quantitative RT-PCR (Taqman) Analysis

Ethical approval for the normal and tumour breast samples was obtained at surgery (University of Oxford, UK). Other tissue samples were from Peterborough Tissue Bank (Peterborough, UK). Real time RT-PCR was used to quantitatively measure MAL2 expression in breast tumour tissues and matched controls. Ethical approval for the normal and tumour breast samples was obtained at surgery (University of Oxford, UK). The primers used for PCR were as follows:

Sense, 5'- tgatgctaactggaacttcctg - 3', (SEQ ID NO:4)
Antisense, 5'- gacccaaactgcaaccataaca - 3' (SEQ ID NO:5)

Reactions containing 5ng cDNA, SYBR green sequence detection reagents (PE Biosystems) and sense and antisense primers were assayed on an ABI7700 sequence detection system (PE Biosystems). The PCR conditions were 1 cycle at 50°C for 2 min, 1 cycle at 95°C for 10 min, and 40 cycles of 95°C for 15s, 60°C for 1min. The accumulation of PCR

product was measured in real time as the increase in SYBR green fluorescence, and the data were analysed using the Sequence Detector program v1.6.3 (PE Biosystems). Standard curves relating initial template copy number to fluorescence and amplification cycle were generated using the amplified PCR product as a template, and were used to calculate MAL2 copy number in each sample.

Relatively low expression levels of MAL2 were seen in normal tissues, Figure 3). In contrast, levels of MAL2 expression were greatly increased in breast tumour samples relative to their matched controls with 7/7 samples showing increased expression levels (Figure 3). In addition, MAL2 expression was increased in 8/13 colon cancer tissues compared to matched normal tissue, and in colon cancer-derived cells lines (Figure 4). MAL2 expression was also increased in liver tumour samples compared to matched normal tissue and hepatocellular- and liver adenocarcinoma-derived cell lines (Figure 4).

Example 3. Immunocytochemistry of MAL2 in HepG2 Cells

Immunocytochemical analysis was carried out on the hepatic carcinoma cell line, HepG2, using a polyclonal antibody, AEP014, raised by immunizing rabbits with the Mal2 specific peptide, NTTITGQPLLSDNQYNIN (SEQ ID NO:6; Covalab). Cells seeded into 8-well chamber slides were maintained at 37°C and 5%CO2 for 48 hours before washing in PBS. Cells were fixed with 4% paraformaldehyde and blocked with 5% donkey serum/PBS, prior to the addition of AEP014. Following a 1hr incubation at RT with AEP014, the cells were washed with 5%donkeyserum/PBS, and incubated for 1hr at RT with a biotin-conjugated secondary antibody (Biotin-SP Affinipure Donkey anti-rabbit, Jackson Immunoresearch), washed with 5%donkeyserum/PBS, incubated with ExtrAvidin-Cy3 (Sigma) for 30min at room temperature, and then processed for fluorescence microscopy.

AEP014-specific plasma membrane staining was seen on HepG2 cells. The staining was restricted to discrete areas of the plasma membrane, rather than a uniform staining of the cell membrane, suggesting that MAL2 is localized to discrete plasma membrane domains, for example, lipid rafts. AEP014 staining was observed on cells that had not been permeabilised, indicating that AEP014 detects an extracellular epitope.

Example 4. Cloning of Mal2 cDNA from Normal Colon

An ORF encoding the Mal2 polypeptide was amplified from colon cDNAs (BD Clontech) by PCR, using Herculase Hotstart DNA polymerase (Stratagene) and the following primers: Mal2 sense 5'-agcggcagcggcagcatgtcg -3' (SEQ ID NO:7) and Mal2 antisense 5'-atacgactgccagtttctaagg -3' (SEQ ID NO:8). The thermal cycling parameters were 1 cycle of

94°C for 3 min, 35 cycles of 94°C for 30s, 55°C for 30s, 72°C for 1 min, and 1 cycle of 72°C for 7 min. PCR products were cloned into a TA cloning vector (pCR4-topo, Invitrogen) and the DNA sequence identified (Figure 2b; SEQ ID NO:3).

These data suggest that MAL2 is expressed in stomach, colon and liver tumour-derived cell lines and shows increased expression in liver, colon and breast cancers. Additionally, MAL2 is shown to be exposed on the surface of cells. These data indicate that MAL2 is of utility as a marker for diagnosis of, and a target for therapeutic intervention in liver cancer, stomach cancer, breast cancer and/or colon cancer.